

Query No.	Score	Length	ID	Description
1	960	99.5	187	AuY21991 Human con
2	893	92.5	175	AuU76866 Human int
3	890	92.2	175	AuU76865 Human int
4	534	55.3	176	AuY21992 Human com
5	333.5	34.6	187	AuB78816 Human com
6	286.5	29.7	184	AuY82349 Human CD1
7	286.5	29.7	184	AuB78832 Human CD1
8	286.5	29.7	184	AuB78832 Human CD1
9	286.5	29.7	184	AuB78832 Human CD1
10	286.5	29.7	184	AuB78832 Human CD1
11	282.5	29.3	180	AuB78832 Human int
12	281.5	29.2	184	AuY82340 Human int
13	281.5	29.2	184	AuB83956 Human CD
14	281.5	29.2	184	AuB83937 Human int
15	276.5	28.7	184	AuU76848 Human int
16	276.5	28.7	184	AuU76857 Human int
17	262	27.9	181	AuB52684 Human int
18	231	23.2	178	AuB08817 A von Will
19	197.5	19.7	180	AuB54907 Von Wille
20	197.5	19.7	180	AuB54907 Von Wille
21	171	17.7	33	AuB02282 Human bet
22	171	17.7	33	AuB02282 Human bet
23	162.5	16.8	180	AuB85598 Mouse pro
24	160.5	16.1	180	AuB85598 Mouse pro
25	155.5	16.6	160	AuB32500 Human bet
26	155.5	16.1	160	AuB32500 Human bet
27	155.5	16.1	160	AuB08816 A von Will
28	155.5	16.1	160	AuB08816 A von Will
29	155.5	16.1	160	AuB08816 A von Will
30	155.5	16.1	160	AuB08816 A von Will
31	155.5	16.1	160	AuB08816 A von Will
32	155.5	16.1	160	AuB08816 A von Will
33	155.5	16.1	160	AuB08816 A von Will
34	155.5	16.1	160	AuB08816 A von Will
35	155.5	16.1	160	AuB08816 A von Will
36	155.5	16.1	160	AuB08816 A von Will
37	155.5	16.1	160	AuB08816 A von Will
38	155.5	16.1	160	AuB08816 A von Will
39	155.5	16.1	160	AuB08816 A von Will
40	155.5	16.1	160	AuB08816 A von Will
41	155.5	16.1	160	AuB08816 A von Will
42	155.5	16.1	160	AuB08816 A von Will
43	155.5	16.1	160	AuB08816 A von Will
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45	155.5	16.1	160	AuB08816 A von Will
46	155.5	16.1	160	AuB08816 A von Will
47	155.5	16.1	160	AuB08816 A von Will
48	155.5	16.1	160	AuB08816 A von Will
49	155.5	16.1	160	AuB08816 A von Will
50	155.5	16.1	160	AuB08816 A von Will
51	155.5	16.1	160	AuB08816 A von Will
52	155.5	16.1	160	AuB08816 A von Will
53	155.5	16.1	160	AuB08816 A von Will
54	155.5	16.1	160	AuB08816 A von Will
55	155.5	16.1	160	AuB08816 A von Will
56	155.5	16.1	160	AuB08816 A von Will
57	155.5	16.1	160	AuB08816 A von Will
58	155.5	16.1	160	AuB08816 A von Will
59	155.5	16.1	160	AuB08816 A von Will
60	155.5	16.1	160	AuB08816 A von Will
61	155.5	16.1	160	AuB08816 A von Will
62	155.5	16.1	160	AuB08816 A von Will
63	155.5	16.1	160	AuB08816 A von Will
64	155.5	16.1	160	AuB08816 A von Will
65	155.5	16.1	160	AuB08816 A von Will
66	155.5	16.1	160	AuB08816 A von Will
67	155.5	16.1	160	AuB08816 A von Will
68	155.5	16.1	160	AuB08816 A von Will
69	155.5	16.1	160	AuB08816 A von Will
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73	155.5	16.1	160	AuB08816 A von Will
74	155.5	16.1	160	AuB08816 A von Will
75	155.5	16.1	160	AuB08816 A von Will
76	155.5	16.1	160	A

AC AB78816;
 XX 29-JUL-2002 (first entry)
 XX Von Willebrand factor type A domain protein SEQ ID NO:38.
 XX Human, NOVX; cystostatic; antiarteriosclerotic; cardiovascular; lymphoma;
 XX anti-diabetic; anti-atherosclerotic; anti-angiogenic; anti-cancer; anti-
 XX cardiomyopathy; atherosclerosis; cell signal processing; diabetes; AIDS;
 XX metabolic pathway modulation; neoplastic; neurological disorder; asthma;
 XX adenocarcinoma; prostate cancer; uterus cancer; immune response;
 XX Crohn's disease; multiple sclerosis; Graft versus host disease.
 XX Unidentified.
 XX WO200230974-A2.
 XX 18-APR-2002.
 XX 12-OCT-2001; 2001WO-US011922.
 XX 12-OCT-2000; 2000US-0240113P.
 XX 16-OCT-2000; 2000US-0240625P.
 XX 16-OCT-2000; 2000US-0240637P.
 XX 16-OCT-2000; 2000US-0240648P.
 XX 16-OCT-2000; 2000US-0240662P.
 XX 16-OCT-2000; 2000US-0240669P.
 XX 16-OCT-2000; 2000US-0240701P.
 XX 16-OCT-2000; 2000US-0240722P.
 XX 16-OCT-2000; 2000US-0240732P.
 XX 18-JAN-2001; 2001US-0262455P.
 XX (CURA-) CURAGEN CORP.
 XX (MILL/) MILLET I.
 XX Grosse WM, Alsobrook JP, Lepley DM, Burgess CE, Mishra V;
 XX Kudara R, Li L, Padiguru M, Shinkets RA, Zerhusen BD, Spytek KA;
 XX Edinger S, Gerlach V, Macdougall J, Stone D, Gunther E, Ellerman K;
 XX WPI; 2002-444172/47.
 XX New NOVX polypeptides and polynucleotides, useful for treating or
 XX preventing a NOVX-associated disorder or a pathological state in a
 XX subject, particularly a human, e.g. cardiomyopathy, atherosclerosis,
 XX cancer or diabetes.
 XX Disclosure; Page 62; 227pp; English.

XX 90 Sequence 176 AA;
 XX Query Match 34.6%; Score 333.5; DB 5; Length 176;
 XX Best Local Similarity 43.4%; Pred. No. 2.8e-28;
 XX Matches 79; Conservative 29; Mismatches 65; Indels 9; Gaps 4;
 XX
 XX 7 DIAPLIDSGSIIIPHPERKKEFTVWQLK--KSKTLFSLMOYSSEPRIHFTKEPON 64
 XX 1 DIVFLIDSGSIIIPHPERKKEFTVWQLK--KSKTLFSLMOYSSEPRIHFTKEPON 60
 XX 65 NNPRLSLVPTIOL-LGTHATGIRKVRKVELFNITNGARKNAFKILVITDGSKFDPPL 123
 XX 61 KDEVLQARKIQQYGGSGTNGTALQYVVRNLTFEASGREGAPKVLVITDGSQDDPI 120
 XX 124 GYEDVTPADREGIVYVUGDAPFRSKROBLNTIASPPEDHVFQNNFEALKTION 183
 XX 121 --RDVLNELLKAGVYVFWALGVGNQNVG-----ELREIASKEDEQVFKVDSFEALDTQE 174
 XX 184 QL 185
 XX 175 LL 176
 XX
 XX RESULT 6
 XX AAY82349
 XX ID AAY82349 standard; protein; 184 AA.
 XX AC AAY82349;
 XX DT 22-JUN-2000 (first entry)
 XX DE Human CD11a I-domain amino acid sequence SEQ ID NO:7.
 XX Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
 XX antitumour; antiviral; inflammation; immunological response; LFA-1;
 XX lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
 XX inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
 XX viral infection; transplant rejection; graft rejection.
 XX Homo sapiens.
 XX US6037454-A.
 XX 14-MAR-2000.
 XX 20-NOV-1997; 97US-00974899.
 XX 27-NOV-1996; 96US-0031971P.
 XX (GETH) GENENTECH INC.
 XX Jardieu PM, Presta LG;
 XX WPI; 2000-282241/24.
 XX New humanized anti-CD11a antibody, useful for treating or preventing e.g.
 XX inflammation and transplant rejection, contains human heavy variable
 XX region complementarity determining regions.
 XX Example; Fig 2; 38pp; English.
 XX The present invention describes a humanised anti-CD11a antibody (Ab) that
 XX binds specifically to the human CD11a I-domain. The Ab has anti-
 XX inflammatory, immunosuppressant, antitumour and antiviral activities. The
 XX Ab blocks lymphocyte function-associated antigen (LFA-1) which is
 XX involved in leucocyte adhesion associated with inflammatory and
 XX immunological responses. The Ab are used: (i) optionally when coupled to
 XX a cytotoxin, to treat or prevent disorders mediated by lymphocyte
 XX function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
 XX inflammatory bowel disease, eczema, systemic lupus erythematosus,
 XX leukaemia, viral infection, transplant rejection and many others also for
 XX inhibiting Graft rejection; (ii) when labeled, to detect CD11a; (iii) for


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80 Sequence 184 AA;
Query Match 29.7%; Score 286.5; DB 8; Length 184;
Best Local Similarity 33.0%; Pred. No. 4,8e-23;
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;
OY 7 DIAFLDGGSGIIIPHDPRMKEFVSTVMEQLKKSTLPSLMQYSEPRHPTFKFQNP 66
DB 5 DLVLFDCGMSLQDFQKILDFMKDKVKKLSNTSYQPAVQFSTSYKTEFDFDYVKR 64
OY 67 WPSLVKPIITOLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFDPLGYE 126
DB 65 DPVLPADREGVIRVIGVDAPFSEKSEKSLNTASKPRDRHVPQNNPEALNTIONLR 186
OY 127 DVLPADREGVIRVIGVDAPFSEKSEKSLNTASKPRDRHVPQNNPEALNTIONLR 186
DB 123 DAAKD-----IIRYIGIKGFQTKESQETLHKFASKPASEVKILDTFEKLDLPTELQ 177
OY 187 KK 188
DB 178 KK 179

RESULT 10
ADRI23224
ID ADRI23224 standard; protein; 187 AA.
AC ADRI23224;
DT 04-NOV-2004 (first entry)
DE Human integrin CD11a alpha subunit A domain.
KW Human; integrin; CD11a; inflammation; antiinflammatory; vasotropic.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Domain 1..184 /label = A_domain
XX Misc-difference 182
XX /note= "Invariant Ile residue"
XX WO2004066914-A2.
XX 12-AUG-2004.
XX 12-MAY-2003; 2003WO-US014919.
XX 10-MAY-2002; 2002US-0014259.
XX (GRHO ) GEN HOSPITAL CORP.
XX Arnaout MA, Li R, Xiong J;
XX WPI; 2004-593980/57.
XX GENBANK; AAC31672.
XX Novel variant integrin CD11b alpha subunit polypeptide, useful for
XX determining candidate compound for binding to CD11b, and for determining
XX compound as activation-dependent ligand.
XX Disclosure; SEQ ID NO 4; 128pp; English.
XX The present sequence is that of the human integrin alpha subunit CD11a A
XX domain (amino acids 150-333 of the full-length protein). This includes an
XX invariant Ile residue. The invention features variant integrin alpha
XX subunit polypeptides in which the invariant Ile is substituted by Gly,
XX Ala or some other amino acid (e.g. Val) or is deleted. The polypeptide
XX can include part or all of the A domain. Replacing the invariant Ile
XX creates a variant integrin polypeptide that is more active (i.e. in
XX structure, a greater proportion of ligand-forming polypeptides than
XX the wild-type form of the subunit. Variant integrin polypeptides of the
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CC invention are useful in assays for compounds that bind to a variant
CC ligand, that interfere with or enhance the binding of an integrin ligand
CC to integrin, and for identifying activation-specific ligands. They are
CC also useful for generating antibodies, e.g. monoclonal antibodies, which
CC recognize the high efficiency form of an integrin. Some such antibodies
CC recognize the high efficiency form of an integrin. Some such antibodies
CC recognize that is in a lower affinity conformation. The invention also
CC provides methods of administering a variant integrin polypeptide, or an
CC antibody that selectively binds it, to identify a ligand which binds to
CC an active integrin. Such assays are useful for diagnosing inflammation,
CC e.g. occult inflammation (e.g. abscess or an active arteriosclerotic
CC lesion). Variant integrin polypeptides can also be used to affect the
CC bioavailability of a variant integrin polypeptide ligand and to treat
CC disorders associated with aberrant or unwanted integrin expression or
CC activity, such as atherosclerosis. A variant CD11a A domain containing an
CC invariant Ile residue is also useful for identifying activation-specific
CC dependent ligand (CD11a) in an ELISA assay. No binding was observed the
CC wild-type protein. Claimed polypeptides comprise: amino acids 150-331 of
CC the CD11a alpha subunit sequence in which the Ile residue at position 331
CC is replaced by Gly or Ala; and amino acids 150-330 of the CD11a alpha
CC subunit but not amino acids 331-1223 of CD11a.
XX
XX Sequence 187 AA;
Query Match 29.7%; Score 286.5; DB 8; Length 187;
Best Local Similarity 33.0%; Pred. No. 4,8e-23;
Matches 62; Conservative 49; Mismatches 70; Indels 7; Gaps 2;
OY 1 CPQSDIAFLDGGSGIIIPHDPRMKEFVSTVMEQLKKSTLPSLMQYSEPRHPTFK 60
DB 1 CIKGNVLFVLFDCGMSLQDFQKILDFMKDKVKKLSNTSYQPAVQFSTSYKTEFDF 60
OY 61 EFQNNPRLSVKPIITOLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 61 DYVKKDPDALLGVHMLLTNTGAINVATEVFEELGAPDPAKTLIIITDGE--A 118
OY 121 DPLGVETVPADREGVIRVIGVDAPFSEKSEKSLNTASKPRDRHVPQNNPEALNT 180
DB 119 TSGNVDAAKD-----IIRYIGIKGFQTKESQETLHKFASKPASEVKILDTFEKLD 173
OY 181 IONLR 188
DB 174 LFTLEQKK 181

RESULT 11
ABR76376
ID ABR76376 standard; protein; 180 AA.
AC ABR76376;
DT 22-AUG-2002 (first entry)
DE Lymphocyte function associated antigen-1 I domain.
KW Lymphocyte function associated antigen-1; LFA-1; human;
XX alpha/beta protein; ligand binding.
XX OS Homo sapiens.
XX WO2002021511-A2.
XX 18-APR-2002.
XX 12-OCT-2001; 2001WO-US032047.
XX 12-OCT-2000; 2000US-0239750P.
XX (IC09-) ICOS CORP.
XX Stauton DE;
XX WPI; 2002-471361/50.
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XX Modulating binding interactions between alpha/beta proteins comprising
PT allosteric regulatory sites, and a binding partner, by contacting with an
PT allosteric effector molecule that interacts with the regulatory site.

XX Disclosure, Fig 1; 163pp; English.

XX The present sequence is the protein sequence of the integrin (I) domain
CC of lymphocyte function associated antigen-1 (LFA-1). The invention
CC provides methods of modulating the binding interaction of a first
CC molecule, which is not LFA-1 or an I domain-containing fragment of LFA-1,
CC and a binding partner. The first molecule has an alpha/beta domain
CC structure comprising an allosteric regulatory site. Modulation of the
CC binding interaction involves contacting with an allosteric effector
CC molecule that interacts with the regulatory site. In vivo methods are
CC expected to alleviate and/or prevent pathological states arising from
CC aberrant binding activity. Methods for identifying modulators are also
CC provided.

XX Sequence 180 AA;

Query Match 29.3%; Score 282.5; DB 5; Length 180;
Best Local Similarity 33.5%; Pred. No. 1.3e-22;
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;

Oy 7 DIAPLIDSGSIIHDFPRMKEPVSTVNEOLKKSKTFLSLMOYSEPRFIHPTFKFQNP 66
Db 4 DLVFLDGSNSLQDFEOKILDPKDWKKLSNTSYQFNAVFSTSYKTEFDFSDYVK 63

Oy 67 NPRLVKEPTOLLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYE 126
Db 64 DPDALLEHVKHMLLNTFGAINVYATEVFREELGARPDPATKVLIIITDGS--ATDSGNI 121

Oy 127 DVIPEDREGVIRYVIGVDAPRSEKRSQSLMTATSKPRDRHVFQVNNFEALKTIONQLR 186
Db 122 DAAKD-----IIRYIIGIGHPOTKESQETLHKFASKPASEFVKILDTFEKLDFELQ 176

Oy 187 EK 188

Db 177 KK 178

RESULT 12

ID AAY82350 standard; protein; 184 AA.

XX AAY82350;

XX 22-JUN-2000 (first entry)

XX Rheus CD11a I-domain amino acid sequence SEQ ID NO:8.

XX Humanized; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
XX antitumor; antiviral; inflammation; immunological response; LFA-1;
XX lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
XX inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
XX viral infection; transplant rejection; graft rejection.

XX Macaca mulatta.

XX US6037454-A.

XX 14-MAR-2000.

XX 20-NOV-1997; 97US-00974899.

XX 27-NOV-1996; 96US-0031971P.

XX (GETH) GRNENTECH INC.

XX Jardieu PM, Presta LG;

XX WPI; 2000-282241/24.

XX New humanized anti-CD11a antibody, useful for treating or preventing e.g.
PT inflammation and transplant rejection, contains human heavy variable
PT region complementary determining regions.

XX Example; Fig 2; 38pp; English.

XX The present invention describes a humanized anti-CD11a antibody (Ab) that
CC binds specifically to the human CD11a I-domain. The Ab has anti-
CC inflammatory, immunosuppressant, antitumor and antiviral activities. The
CC Ab blocks lymphocyte function-associated antigen (LFA-1) which is
CC involved in leucocyte adhesion associated with inflammatory and
CC immunological responses. The Ab are used: (i) optionally when coupled to
CC a cyclosporin, to treat or prevent allograft rejection; (ii) optionally
CC in combination with cyclosporin, to treat or prevent diseases such as
CC psoriasis, leukaemia, viral infections, systemic lupus erythematosus,
CC rhinitis, leukaemia, eczema, and many others, also for
CC inhibiting graft rejection; (iii) when labeled, to detect CD11a; (iii) for
CC tumor pretreatment; (iv) for delivery of enzymes that convert prodrugs
CC to active anticancer agent; and (v) for affinity chromatography. The Ab
CC retain about the same activity in adhesion and mixed lymphocyte response
CC assays as the murine antibodies from which they are derived. The murine
CC anti-CD11a antibody MPM24 has IC50 0.09 nM for preventing adhesion
CC between Jurkat cells (expressing LFA-1) and normal epidermal leucocyte-1.
CC Keratinocytes that express LFA-1. The present invention also provides
CC the full sequence of the amino acid sequence of the murine CD11a I-domain,
CC which is used in the exemplification of the present invention.

XX Sequence 184 AA;

Query Match 29.2%; Score 281.5; DB 3; Length 184;
Best Local Similarity 33.0%; Pred. No. 1.7e-22;
Matches 60; Conservative 48; Mismatches 67; Indels 7; Gaps 2;

Oy 7 DIAPLIDSGSIIHDFPRMKEPVSTVNEOLKKSKTFLSLMOYSEPRFIHPTFKFQNP 66
Db 5 DLVFLDGSNSLQDFEOKILDPKDWKKLSNTSYQFNAVFSTSYKTEFDFSDYVK 64

Oy 67 NPRLVKEPTOLLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYE 126
Db 65 DPDALLEHVKHMLLNTFGAINVYATEVFREELGARPDPATKVLIIITDGS--ATDSGNI 122

Oy 127 DVIPEDREGVIRYVIGVDAPRSEKRSQSLMTATSKPRDRHVFQVNNFEALKTIONQLR 186
Db 123 DAAKD-----IIRYIIGIGHPOTKESQETLHKFASKPASEFVKILDTFEKLDFELQ 177

Oy 187 EK 188

Db 178 KK 179

RESULT 13

ID ADG38996 standard; protein; 184 AA.

XX ADG38996;

XX 26-FEB-2004 (first entry)

XX Monkey CD11a I-domain.

XX Monkey; CD11a; I-domain; monoclonal antibody;
XX cluster of differentiation 11a; mixed lymphocyte response assay;
XX Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
XX ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
XX psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
XX rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
XX diabetes mellitus; prodrug activating enzyme.

XX Macaca mulatta.

XX US20020207336-A1.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2005, 17:08:58 ; Search time 38 Seconds
(without alignments)
476.020 Million cell updates/sec

Title: US-09-758-493-1_COPY_1_188
Perfect score: 965
Sequence: 1 CPQEDSDIAFLDGGSIIP.....VFQVNFPAKLTIONLAKK 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 95191

Minimum DB seq length: 0
Maximum DB seq length: 188

Post-processing: Minimum Match 04
Maximum Match 1004
Listing first 45 summaries

Database : PIR 79:
1: piri:
2: piri2:
3: piri3:
4: piri4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	81	8.4	170	B53274	complement factor
2	78.5	8.1	166	JT0358	hypothetical prote
3	73.5	7.5	187	A83255	hypothetical prote
4	71.5	7.2	169	B70474	ribosomal protein
5	71.5	7.4	169	B70474	hypothetical prote
6	70.5	7.3	181	G64307	hypothetical prote
7	70.5	7.3	187	AF0255	probable phage pro
8	69.5	7.2	141	A82880	ribosomal protein
9	69.5	7.2	146	H97788	hypothetical prote
10	68.5	7.1	90	H69159	hypothetical prote
11	67.5	7.0	172	I38424	centrin - human
12	67.5	7.0	175	A64330	hypothetical prote
13	67	6.9	150	C71706	hypothetical prote
14	66	6.9	171	A98901	uncharacterized co
15	66	6.9	171	A98901	hypothetical prote
16	65.5	6.8	152	G5453	hypothetical prote
17	65.5	6.8	172	S38531	uncharacterized co
18	65.5	6.8	180	C90526	conserved hypothet
19	65	6.7	132	PMPEL	H+-transporting tw
20	65	6.7	155	A84021	modulation of CheA
21	65	6.7	164	T10726	calmodulin - green
22	65	6.7	172	AH2456	hypothetical prote
23	64.5	6.7	150	1 MORTA2	myosin alkali ligh
24	64.5	6.7	159	2 AC2254	hypothetical prote
25	63.5	6.6	120	A64435	hypothetical prote
26	63.5	6.6	159	2 AC2254	hypothetical prote
27	63.5	6.6	158	C93847	probable phage pro
28	63.5	6.6	165	2 G81324	probable phage pro
29	63	6.5	127	B70022	acylate catabolis

ALIGNMENTS

RESULT 1

B53274
Complement factor B subunit Bb - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 09-May-2004
E:Accession: B53274
E:Protein: B. Van de Veghe, A.R.; Coppeters, W.R.; Van Zeveren, A.J.; Bouquet, Y.
Immunogenetics 34, 192-195, 1991
A:Title: Cloning and sequencing of the porcine complement factor B.
A:Reference number: A53274; MUID:91372866; PMID:1680099
A:Accession: B53274
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-170 <PEE>
A:Note: sequence extracted from NCBI backbone (NCBI:56036, NCBI:P.56043)
C:Superfamily: complement B/C2; complement factor H repeat homology; trypsin homology

Query Match 8.44; Score 81; DB 2; Length 170;
Best Local Similarity 22.04; Pred No. 7.7; Indels 38; Gaps 8;
Matches 38; Conservative 33; Mismatches 33

Qy	41	KTLFLMOYSEFRHFTFKFQNNPNSL-VKPIITQLG-----RHTATGIRKV 92
Db	7	KPKGLVTVATDPKLVRS-----NPKSADADWVTQLOKISYDDHKLKAGTNTKAL 60
Qy	93	RELPMITNGARN-----AFKLWITDG--EKFGDPLGYEDVIPADREGVIR---- 139
Db	61	LEVYNNMGVNPQNNTRHVLVLTGLNMGDSVTVIDSLNLTNGDKRNP 120
Qy	140	-----YVIGVDGDAFSEKROELNTAKSPRD--HVFQNNPRAKLTIONOL 185
Db	121	EDYLDIYVGVGVLNVQK-----NINALASKKQKQVFKLKDVLNLESDVFPOM 169

RESULT 2

JT0358
Hypothetical protein g6 (rep 3', region) - Clostridium perfringens plasmid pIP404
C:Species: Clostridium perfringens
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
E:Accession: JT0358
E:Protein: Clostridium perfringens S.T.
Plasmid 19, 134-140, 1988
A:Title: Complete nucleotide sequence and genetic organization of the bacteriocinogen
A:Reference number: JT0353; MUID:88336297; PMID:2901768
A:Accession: JT0358
A:Molecule type: DNA
A:Residues: 1-166 <GAR>
A:Cross-references: UNIPROT:P18017; GB:M32882; GB:J03309; NID:g150738; PID:AAA98252..
C:Genetic:
A:Genome: plasmid
Query Match 8.14; Score 78.5; DB 2; Length 166;

A:Cross-references: UNIPROT:027130; GB:AE000666; NID:g5622140; PION:AA8
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1056
C:Superfamily: ribosomal protein S7/S5

Query Match 7.5%; Score 72.5; DB 2; Length 186;
Best Local Similarity 22.1%; Pred. No.46;
Matches 38; Conservative 29; Mismatches 52; Indels 53; Gaps 8;

Qy 4 RSDIAFLIDGSGIIIPHDPRMKPEPVSTVMQOLKSKTFLSLMOYSEEPRIHFTKEFO 63
Db 16 EDMLAKVLCIDSLVPHTWGR-----HVCRQFAKSK----- 48

Qy 64 NNPNPSLVKPIITOLLGRTHATGIR-----KVRELPHNIT-GARKNAFKILWITDGB- 117
Db 49 -----SIVRELINKWRTKSNRKNVAKYVQEAFLNRTKRNKQIVLIVAVENTS 102

Qy 118 -----KFCDDPLGVE-----GVYDEADRGVIRVVI-----GVGDAPPSKSGRQ 156
Db 103 PREETRIKYG-IGYQAVVDISPRVDSLGPIITRGAMAAFAFNKKSITB 153

RESULT 5

hypothetical protein sq_2028 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Dates: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
A:Accession: F70470
V:Reckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Graham, D.E.;
Nature 392, 353-358, 1998

A>Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:981956666; PMID:9537320
A:Accession: B70474
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-169 <Q>
A:Cross-references: UNIPROT:067822; GB:AE000768; NID:g2984249; PION:AAAC
A:Experimental source: strain VP5
A:Gene: sq_2028
C:Superfamily: Archaeoglobus hypothetical protein AF1244

Query Match 7.4%; Score 71.5; DB 1; Length 169;
Best Local Similarity 23.5%; Pred. No.50;
Matches 36; Conservative 24; Mismatches 58; Indels 35; Gaps 6;

Qy 14 GSGSIIIPHDPRMKPEPVSTVMQOLKSKTFLSLM-OYSEEPRIHFTKPFQNNPNRS-- 70
Db 29 GEULIITHNCRRLYL--VEBEEBSPCVSTREAREALGFLLAGITFQVTERMEL 86

Qy 71 LVKPI-----TQLGRTHATGIRKVVRELPHNITGARKNAFKILWITDTSKRG 120
Db 87 LMKSIYVWKKVGNSENPFIKTIADLR-----RKTGVSIILIRDEMIIP 133

Qy 121 DPLYEDVTPAD-----RGVIRVITGVD 146
Db 134 SDPTFKELQGDILVVGTRQLIKLEMGCD 166

RESULT 6

G64307
hypothetical protein M3063 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Dates: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
A:Accession: G64307
R:Bult, C.J.; White, O.; Olson, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blal
; Reich, C.I.; Overbeek, A.; Kirkness, E.F.; McIninch, K.C.; Merrick, J.M.; Glodke,
gen, J.D.; Olsen, L.P.; Hama, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
; Klenk, H.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Kl, S.; Church, G.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: H6159
 A:Molecule type: DNA
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Residues: 1-90 <MTH>
 A:Cross-references: UNIPROT:O26558; GB:AE000830; GB:AE000666; NID:g2621523; PIDN:AAB8496
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH458

Query Match 7.1%; Score 68.5; DB 2; Length 90;
 Best Local Similarity 23.8%; Pred. No. 41;
 Matches 24; Conservative 16; Mismatches 30; Indels 31; Gaps 5;

Qy 1 CPQSDIPLDGGSGIIPHDPRKPEFVSTWEOQKSKTLFLSMQYSEFRHPTPK 60
 Db 13 CDAAEDTVT-----GATEIL-----RVDTYET-KEKLRSQNYRAI----- 49

Qy 61 EPQNNPNSLVKPIPTQLGTHATGIRKVRLEFNITNG 101
 Db 50 --FENRATP-----TAITDREWNITGTVNRFELFVDEG 82

RESULT 11

138424 - human
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
 C:Accession: 138424
 R:Erabolu, R.; Sanders, M.A.; Salisbury, J.L.
 J. Cell Sci. 107, 9-16, 1994
 A:Title: Cloning of a cDNA encoding human centrin, an EF-hand protein of centrosomes and
 A:Reference number: 138424; MUID:94230620; PMID:8175926
 A:Accession: 138424
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-148
 A:Cross-references: UNIPROT:Q12798; EMBL:U01270; NID:g3337234; PIDN:AC27343.1; PID:g414
 C:Superfamily: calmodulin; calmodulin repeat homology
 C:Keywords: EF hand
 P:28-60/Domain: calmodulin repeat homology <EF1>
 P:64-96/Domain: calmodulin repeat homology <EF2>
 F:101-133/Domain: calmodulin repeat homology <EF3>
 F:137-169/Domain: calmodulin repeat homology <EF4>

Query Match 7.0%; Score 67.5; DB 2; Length 172;
 Best Local Similarity 25.6%; Pred. No. 16+02;
 Matches 33; Conservative 25; Mismatches 54; Indels 17; Gaps 6;

Qy 10 FLIDGSGIIPHDPRKPEFVSTWEOQKSKTLFLSMQYSEFRHPTKSFQNNPR 69
 Db 40 FVDGSGTI---DAKELVAMRALGFEPKKEKMKMSRVDRGTGKISFNDF----- 89

Qy 70 SLVKPIPTQLGTHATGIRKVRLEFNITNGARNAPKILVITD--GSKFGDPLGYED 127
 Db 90 --LAVNTQKSEKUTKEELKAFR-LPD--DDETKISFKNLKVAVNELGENUTDE-ELGE 144

Qy 128 VPEADREG 136
 Db 145 MIDEADREG 153

RESULT 12

A64330
 hypothetical protein MJ0240 - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
 C:Accession: A64330
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,

; Reich, C.I.; Overbeek, R.; Kirkness, S.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, S.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
 A:Title: Complete genome sequence of the hyperthermophilic ciliated protozoan, Methanococcus jannaschii
 A:Reference number: A64300; MUID:96317999; PMID:8688087
 A:Accession: A64330
 A:Molecule type: DNA
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Residues: 1-175 <BUL>
 A:Cross-references: UNIPROT:Q57692; GB:U67479; GB:L177117; NID:g1590965; PIDN:AAB98225
 C:Genetics:
 C:Superfamily: Thermophilic adenylate cyclase, CyaB type

Query Match 7.0%; Score 67.5; DB 2; Length 175;
 Best Local Similarity 24.7%; Pred. No. 1.2e+02;
 Matches 41; Conservative 20; Mismatches 64; Indels 41; Gaps 6;

Qy 33 VMEQKSKTFLSMQYSEFRHPTKSFQNNPNSLVKPIPTQLGTHATGIRKVV 92
 Db 16 VVEQKGLGKFKFKGFOFIYFNGIDRDFR-----ETDEALRIDED 58

Qy 93 RELFNITNGAR-----KNAFKILVITDKEFGD---SLGYEVQVTP-----EADRE 135
 Db 59 GIFFVTYKPKDKISKTRIEIVKIDKKNRQIPKLGKFEVPPKIRKIRIYKEDIE 118

Qy 136 GVIRYVIGVDAPFSEKSRQELNTIASKPPRDHVPQVNNFEALKTI 181
 Db 119 ASDIDVEGLGLPLELSEKISIDIN-----EKDKYLE-EMMEILKAL 157

RESULT 13

C71706
 hypothetical protein RP470 - Rickettsia prowazekii
 C:Species: Rickettsia prowazekii
 C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
 R:Anderson, S.G.B.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alenmark
 Nature 396, 133-140, 1998
 A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
 A:Reference number: A71630; MUID:99039499; PMID:9821893
 A:Accession: C71706
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-150 <AND>
 A:Cross-references: UNIPROT:Q92D74; GB:A235271; GB:A235269; NID:g3868717; PIDN:CAA1
 A:Experimental source: strain Madrid 8
 C:Genetics:
 C:Superfamily: Rickettsia prowazekii hypothetical protein RP470

Query Match 6.9%; Score 67; DB 2; Length 150;
 Best Local Similarity 30.5%; Pred. No. 1e+02;
 Matches 18; Conservative 11; Mismatches 28; Indels 2; Gaps 2;

Qy 62 FQNNPNSLVKPIPTQLGTHATGIRKVRLEFNITNGARNAPKILVITDKEFG 120
 Db 58 IQNKSTPQSFPTSLDTEHKEAA-RSVIKELKVTI-ANQAKYKELIILASPKMLG 114

RESULT 14

A96901
 uncharacterized conserved protein, ortholog of YRKA B. subtilis CAC0009 [imported]
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C:Accession: A96901
 R:Noelling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: A96901

```

A:Status: Preliminary
A:Species: Deinococcus radiodurans
A:Residues: 1-171 <KUR>
A:Cross-references: UNIPROT:Q97N29; GB:AE001437; PIDN:AAK77996.1; PID:gi5022827; GSPDB:G
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0009

Query Match      6.9%; Score 67; DB 2; Length 171;
Best Local Similarity 22.5%; Pred. No. 1.2e+02;
Matches 38; Conservative 23; Mismatches 72; Indels 36; Gaps 6;

QY 50 SEERKHTFFKFNPNP-----RSUKPTQLLQRTHTATGIRKRVREL 95
DB 3 SEERENIKK-LENDPEIKGSTLAGELVGTQVIVADILAKCHKLIATPKY--- 58

QY 96 FNTNGARNAFK-ILVVTDGKFGPLG-----YEDVIPEDREGVIRVIGVD 146
DB 59 --INKNNSIKRVLAVHHERNAIDELNSVIKFGVGVEDVIEHPLYGIRGILMRT 116

QY 147 AFREKSRQELNTIAKP-----PRHVFQVNNFEALKTIONQLREK 188
DB 117 LFDVNFPMKIRDSAEPLSILITGVHLITRTDNEEDMNIVDELTRK 165

RESULT 15
H75433
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: H75433
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
Article: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Accession: H75433; MDID:20036896; PMID:10567286
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <WHI>
A:Cross-references: UNIPROT:Q9RV48; GB:AE001962; GB:AE000513; NID:96458855; PIDN:AAF107C
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1121
A:Map position: 1

Query Match      6.8%; Score 66; DB 2; Length 126;
Best Local Similarity 27.0%; Pred. No. 1e+02;
Matches 34; Conservative 18; Mismatches 50; Indels 24; Gaps 6;

QY 80 GRHTT-----ATGIRKRVRELNTNGARNAFKILVVTDGKFGDPLGYEDVIPED 133
DB 6 GRHTEHEPIRATSMWR-VDOVFLARRGRIEVCISLV-----NDRGGLRLHLSVVAPTDD 60

QY 134 REGVI-----RYVIGVDAP-----RSEKSRQELNTIAKPPHD---HVFQVNNFEALKT 180
DB 61 PAQAVRHAAKFVAGKGNVFSARNARVWREQUITLQDELINDTLEDTTFDEFEETLAA 120

QY 181 IONQLR 186
DB 121 VDELR 126

Search completed: November 14, 2005, 17:38:17
Job time : 40 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2005, 17:05:43 ; Search time 172 Seconds
(without alignments)
559,714 Million cell updates/sec

Title: US-09-758-493-1_COPY_1_188
Perfect score: 965
Sequence: 1 CPQSDIAFLDGGSGIIP.....VFQVNFALKTIONQREK 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues 609828
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 188

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:
1: uniprot_sprot;
2: uniprot_trembl;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	293	30.4	79	2 Q8HY27	Q8HY27 ovis aries
2	293	30.4	79	2 Q8HY41	Q8HY41 bos taurus
3	127.5	13.2	156	2 Q71V33	Q71V33 homo sapien
4	89	9.2	171	2 Q6AP53	Q6AP53 desulfotale
5	82	8.5	184	2 Q63LC8	Q63LC8 burkholderi
6	82	8.5	184	2 Q63LH4	Q63LH4 burkholderi
7	82	8.5	184	2 Q63LH4	Q63LH4 burkholderi
8	80.5	8.3	162	2 Q749A4	Q749A4 geobacillus
9	79.5	8.2	179	2 Q6GV44	Q6GV44 debaryomyces
10	78.5	8.1	166	1 YP16 CLOPE	YP16 clostridium
11	78.5	8.1	166	1 YP16 CLOPE	YP16 clostridium
12	78	8.1	134	2 Q920X7	Q920X7 cavia porce
13	74	7.7	145	2 Q9NLS5	Q9NLS5 plasmodium
14	73.5	7.6	187	2 Q9KAT5	Q9KAT5 bacillus ha
15	72.5	7.5	135	2 Q6LTV3	Q6LTV3 leptospira
16	72.5	7.5	139	2 Q6LTV3	Q6LTV3 leptospira
17	72.5	7.5	139	2 Q6LTV3	Q6LTV3 leptospira
18	72.5	7.5	139	2 Q6LTV3	Q6LTV3 leptospira
19	72.5	7.5	139	2 Q6LTV3	Q6LTV3 leptospira
20	72.5	7.5	139	2 Q6LTV3	Q6LTV3 leptospira
21	72.5	7.5	139	2 Q6LTV3	Q6LTV3 leptospira
22	72.5	7.5	139	2 Q6LTV3	Q6LTV3 leptospira
23	71.5	7.4	168	2 Q7R941	Q7R941 plasmodium
24	71.5	7.4	168	2 Q7R941	Q7R941 plasmodium
25	71	7.4	127	2 Q7Y2G6	Q7Y2G6 aquifex aeo
26	70.5	7.3	143	2 Q7J373	Q7J373 bos taurus
27	70.5	7.3	143	2 Q7J373	Q7J373 bos taurus
28	70.5	7.3	143	2 Q7J373	Q7J373 bos taurus
29	70.5	7.3	143	2 Q7J373	Q7J373 bos taurus
30	70.5	7.3	143	2 Q7J373	Q7J373 bos taurus
31	70	7.3	159	1 HBLT_GOSHI	HBLT_GOSHI

ALIGNMENTS

RESULT 1	Q8HY27	PRELIMINARY;	PRT;	79 AA.
ID	Q8HY27	PRELIMINARY;	PRT;	79 AA.
AC	Q8HY27	01-MAR-2003 (TrEMBLrel. 23, Created)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)			
DR	Laurel, C. (2003) The ENBL/GenBank/DBJ databases.			
DS	Laurel, C. (2003) The ENBL/GenBank/DBJ databases.			
GN	Name:cd11b; Integrin alpha-M chain (fragment).			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Caprinae; Ovis.			
OX	NCBI_TaxID=9940;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Blood;			
RA	Protein C (OS=Ovis aries, H. Buckmaster R.M., Pfaffel M.W.,			
DR	EMBL: AJ353524; CDAS9479.1; .			
DR	HSP; P1215; 1BHQ.			
DR	GO: GO:0007229; P: integrin-mediated signalling pathway; IEA.			
DR	InterPro: IPR02035; VMP_A.			
DR	Pfam: PF00092; VMA; 1.			
DR	PROSITE: PS0234; VMP_A; 1.			
FT	NON_TER	1		
FT	NON_TER	79		
SQ	SEQUENCE	79 AA; 8602 MW; B4861D27768630D CRC64;		
Query Match	30-44;	Score 293; DB 2; Length 79;		
Best Local Similarity	87.5%;	Pred. No. 1.7e-16;		
Matches	56; Conservative	6; Mismatches 2; Indels 0; Caps 0;		
Oy	125 YEDVIPADREGVIRYIGVDAPFSEKSEKSELNTIASKPPRDHVFQVNFALKTIONQ 184			
Db	1 YEDVIPADRGKIIIRYIGVDAPFSEKSEKSELNTIASKPPRDHVFQVNFALKTIONQ 60			
Oy	185 LREK 188			
Db	61 LREK 64			
RESULT 2	Q8HY41	PRELIMINARY;	PRT;	79 AA.
ID	Q8HY41	PRELIMINARY;	PRT;	79 AA.
AC	Q8HY41	01-MAR-2003 (TrEMBLrel. 23, Created)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)			
DR	Laurel, C. (2003) The ENBL/GenBank/DBJ databases.			
DS	Laurel, C. (2003) The ENBL/GenBank/DBJ databases.			
GN	Name:cd11b; Integrin alpha-M chain (fragment).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

RL Science 302:1967-1969(2003).
CC - I - SIMILARITY. Belongs to the ribosomal protein S5P family

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SO SEQUENCE 179 AA; 20118 MW; 5F34BA42DD342AB9 CRC64;

Query Match      8.24; Score 79.5; DB 2; Length 179;
Best Local Similarity 23.64; Pred. No. 1.1e-02;
Matches 38; Conservative 28; Mismatches 58; Indels 37; Gaps 7;

OY 37 KPVFTVMEQLKKSKTFLFQMQVSEBFFI--HFTKFKFQNP--NPRGLVKPITQLLCRT 82
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 39 KQFSNQLLSQSR---LYSLVTSPEAKLYKYNKXSIINNSAHPDLSLVD----- 86
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY 83 HTATGTGIRVRELFINITNGAKNAKFLIVITD-----SKFDGLGYEDVPIPADREG 136
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY 87 -----VRPEVEYEDGHIIPNAINIPKSSPGALOLSPBEFNNFGFDK--PSKDKEU 135
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY 137 VIRVIVIGVDAPFRSEKSRQELNTASKPRDHVPOVNFPA 177
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY 136 IFYCLAGV-----RSTAABELADTGYKGRGVYGYEDWAA 172
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 10
OCV6FF5 PRELIMINARY: PRT; 151 AA.

ID OCVFF5
AC O6VFF5;
CT AC
DT 05-JUL-2004 (TREMblurel. 27, Created)
DT 05-JUL-2004 (TREMblurel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblurel. 27, Last annotation update)
DE Resistance protein Candidate fragment.
DE Resistance protein Candidate fragment.
DE Eukaryotic Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC OC
OC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
OC Helianthus.
OC NCBI_TaxID=4232;
OC [1]
RN SEQUENCE FROM N.A.
RP PLOCIC A.M.; Layden J.; Kesseli R.V.;
RA Submitted (SEP-2008)73211
RL 131333
DR InterPro:IPR002182; NB-ARC.
DR Pfam: PF00931; NB-ARC; 1.
FT NON TER 1 1
FT FT NON TER 151 151
SO SEQUENCE 151 AA; 17071 MW; A132AA05FC7076F1 CRC64;

Query Match      9.18; Score 78.5; DB 2; Length 151;
Best Local Similarity 29.84; Pred. No. 1.1e-02;
Matches 38; Conservative 21; Mismatches 46; Indels 27; Gaps 9;

OY 33 VMEQLKKGS--KTLFSLMYSSEBPIHFTKFKFQNPNNISLVPITQLLCRT--HTATG 87
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 1 MMEQLKKAAVEDLKMPDLV-----VKVVLGS--NTDPTSLQAKARYIGNTLVETGK 50
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY 88 IR-KVYRELFINITNGAKNAKFLIVITDGEK-----FG-DPL--GYEDVPIPADREGV 137
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY 51 AAARLRKIFEVKSSQOK--KILVIMODIVKEVELDPLGSLPUNGKLLFTSRFENVC 108
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY 138 IRVIVIGVDAPFR 149
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY 109 THMGVIGGSIFR 120
DB      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 11
OCV6F5 YP16_CLOPE STANDARD: PRT; 166 AA.

ID YP16_CLOPE
AC YP1607;
CT AC
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hypothetical 19.7 kDa protein (ORF6).
OC OC Clostridium perfringens.
OC Clostridium perfringens.
OC Plasmid pIP404.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.

```



```
DB 20 PRKSKSFVNOAYMDU-----TSFHYENMKR-KIH-----KNIMNKN-----56
QY 83 HTATGRTVRELVNITNGARKNAFKI 109
DB 57 -----NEK-IQSKNLNLSKENAYKI 78

RESULT 14
ID QSKATS PRELIMINARY: PRT; 187 AA.
AC QSKATS;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DE 832201 (TEMBLrel. 24, Last annotation update)
DE 832201 (TEMBLrel. 24, Last annotation update)
GN OrderedLocusNames=BH2201;
OS Bacillus halodurans;
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125;
RA MEDLINE=20512582; PubMed=1058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Tokaki Y., Maeno G., Sasaki K., Masui N.,
RA Fujikawa K., Kamei C., Nakamura Y., Ogasawara N., Aihara S.,
RA Fujikawa K., Kamei C., Nakamura Y., Ogasawara N., Aihara S.,
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AF001514; BAB05920.1; -.
DR PIR; A83925; A83925.
DR InterPro; IPR007353; DUF421.
DR Pfam; PF04239; DUF421; 1.
KW Complete proteome.
SQ SEQUENCE 187 AA; 21751 MW; 33C0341D633C5836 CRC64;

Query Match 7.6%; Score 73.5; DB 2; Length 187;
Best Local Similarity 22.6%; Pred. No. 3.7e+02;
Matches 38; Conservative 32; Mismatches 59; Indels 39; Gaps 8;

QY 12 IDGSGIIPHDFRMRKVFSTVMEQKKSKTLFSLMOYSEFRH--FTFKFQNNPNR 69
DB 47 LDGTPTLLIQDGKLE-----HNKKEN--FSIDMFQALREKEIFDMQVE-----91
QY 70 SLVVKPTTOLLGRTHATGIRK-----VRELFTNGARKNAFKILVITDQKPGDPLG 124
DB 92 -----TALTDGTGVLVKRPYLPVTRKDLNIPVAKHRPFIUII---DQVKNENLL 142
QY 125 YEDVIPADREGVIRYVGVGDAPRS---EKSROELMTASKPRDHV 169
DB 143 ENDSLEWKLQIBILARGYGIQDVFAVLDSKGLVLDTY-----RHLL 185

RESULT 15
ID QSLTV3 PRELIMINARY: PRT; 135 AA.
AC QSLTV3;
DT 05-JUN-2004 (TEMBLrel. 27, Created)
DT 05-JUN-2004 (TEMBLrel. 27, Last sequence update)
DE 05-JUN-2004 (TEMBLrel. 27, Last annotation update)
DE Hypothetical protein
GN OrderedLocusNames=PBPA0859;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cecchi A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
RA Velli G.
RT "Genome analysis of Photobacterium profundum reveals the complexity of
```

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RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cecchi A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
RA Velli G.
SQ SEQUENCE 135 AA; 14724 MW; 986784595286B333 CRC64;

Query Match 7.5%; Score 72.5; DB 2; Length 135;
Best Local Similarity 25.2%; Pred. No. 3.1e+02;
Matches 27; Conservative 19; Mismatches 32; Indels 29; Gaps 4;

QY 27 KEFVSTVMEQLKSKTLF-----SLMOYS-REPRIHTPKFQNNPN 67
DB 37 KQSVNTSLQLLPGSETHIIFGTSDEGNSRELVCSSALLEYSAEIVKIAFTIKERLDGA 96
QY 68 PRSLVVKPTTOLLGRTHATGIRKVVRELFTNGARKNAFKILVIT 114
DB 97 WRTIISPV-----LSTGLNEPTS--FVSTNDASKEHVKLQVEVT 133

Search completed: November 14, 2005, 17:37:33
Job time : 175 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2005, 17:26:24 ; Search time 43 Seconds
(without alignments)
326.373 Million cell updates/sec

Title: US-09-758-493-1_COPY_1_188
Perfect score: 965
Sequence: 1 CPQDSDIADLDSGSIIP.....VFQVNPFAKTIQNQLREK 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 387217

Minimum DB seq length: 0
Maximum DB seq length: 188

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/5C_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/5D_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/5E_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/5F_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	960	99.5	187	2	US-08-177-109A-61
2	960	99.5	187	2	US-08-687-706-61
3	534	55.3	187	2	US-08-177-109A-62
4	534	55.3	187	2	US-08-687-706-62
5	534	55.3	187	5	PCT-US96-01314-60
6	286.5	29.7	184	3	US-08-974-899-7
7	286.5	29.7	184	4	US-09-795-799-7
8	281.5	28.2	184	3	US-08-974-899-8
9	281.5	28.2	184	3	US-08-974-899-8
10	266	27.6	181	5	US-08-974-899-8
11	171	17.7	33	2	US-08-476-062A-61
12	171	17.7	33	2	US-08-476-062A-61
13	146	15.1	28	2	US-08-476-062A-10
14	146	15.1	28	2	US-08-476-062A-10
15	129	13.4	25	5	PCT-US96-01314-8
16	129	13.4	25	5	PCT-US96-01314-8
17	126	13.1	29	5	PCT-US96-01314-69
18	125	13.0	24	5	PCT-US96-01314-69
19	117	12.1	22	2	US-08-476-062A-12
20	117	12.1	22	2	US-08-476-062A-12
21	113	11.7	22	5	PCT-US96-01314-68
22	113	11.7	22	5	PCT-US96-01314-68
23	113	11.7	22	5	PCT-US96-01314-72
24	112	11.6	21	2	US-08-476-062A-7
25	112	11.6	21	2	US-08-476-062A-7
26	111	11.5	20	5	PCT-US96-01314-65
27	110	11.4	20	2	US-08-476-062A-17

Sequence 17, Appl
Sequence 70, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 62, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 43, Appl
Sequence 73, Appl
Sequence 6, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 56, Appl
Sequence 64, Appl
Sequence 1, Appl
Sequence 71, Appl

ALIGNMENTS

RESULT 1
US-08-177-109A-61
Sequence 61 Application US/08177109A
Patent No. 682615
GENERAL INFORMATION:
APPLICANT: Dennis E. Hourcade and Teresa J. Ogleby
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
STATE: Atlanta
COUNTRY: US
ZIP: 30109-1450
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/177,109A
FILING DATE: 01-JAN-1994
CLASSIFICATION: 214
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: Protein
HYPOTHEICAL: NO
US-08-177-109A-61

Query Match 99.5%; Score 960; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 3.4e-96;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPQDSDIADLDSGSIIPHDPRMRKPFVSTWMOLEKSKTLFSLMQYSEPRHFTFK 60
DB 1 CPQDSDIADLDSGSIIPHDPRMRKPFVSTWMOLEKSKTLFSLMQYSEPRHFTFK 60
QY '61 EFQVNPRLVKEPTQLGCTHTATGIRKVRRELFNITNGARONAKFILVITDGEKFG 120

Db 61 EFQNNPNSLVKPTQLGRTHTATGIRKVVRELNTNGARKNAFKILVITDGKEFG 120
Oy 121 DPLGYEDVPEADREGVIRYVGVGDAPRSEKSRQELNTIASKPPRDHVFQNNFALKT 180
Db 121 DPLGYEDVPEADREGVIRYVGVGDAPRSEKSRQELNTIASKPPRDHVFQNNFALKT 180
Oy 181 IONQLRE 187
Db 181 IONQLRE 187

RESULT 2
US-08-687-706-61
; Sequence 61, Application US/08687706
; Patent No. 5869615
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/687,706
; FILING DATE: 26-JUL-1996
; CLASSIFICATION: 514
; PRIORITY INFORMATION:
; PRIORITY NUMBER: US 08/177,109
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU 107 DIV
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-687-706-61

Query Match 99.5%; Score 960; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 3.4e-96;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTKLFLSLMOYSEEFRIHPTFK 60
Db 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTKLFLSLMOYSEEFRIHPTFK 60
Oy 61 EFQNNPNSLVKPTQLGRTHTATGIRKVVRELNTNGARKNAFKILVITDGKEFG 120
Db 61 EFQNNPNSLVKPTQLGRTHTATGIRKVVRELNTNGARKNAFKILVITDGKEFG 120
Oy 121 DPLGYEDVPEADREGVIRYVGVGDAPRSEKSRQELNTIASKPPRDHVFQNNFALKT 180
Db 121 DPLGYEDVPEADREGVIRYVGVGDAPRSEKSRQELNTIASKPPRDHVFQNNFALKT 180

Oy 181 IONQLRE 187
Db 181 IONQLRE 187
RESULT 3
US-08-177-109A-62
; Sequence 62, Application US/08177109A
; Patent No. 5869615
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/177,109A
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU 107
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-177-109A-62

Query Match 55.3%; Score 534; DB 2; Length 187;
Best Local Similarity 55.6%; Pred. No. 5.4e-50;
Matches 104; Conservative 34; Mismatches 49; Indels 0; Gaps 0;
Oy 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTKLFLSLMOYSEEFRIHPTFK 60
Db 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTKLFLSLMOYSEEFRIHPTFK 60
Oy 61 EFQNNPNSLVKPTQLGRTHTATGIRKVVRELNTNGARKNAFKILVITDGKEFG 120
Db 61 EFQNNPNSLVKPTQLGRTHTATGIRKVVRELNTNGARKNAFKILVITDGKEFG 120
Oy 121 DPLGYEDVPEADREGVIRYVGVGDAPRSEKSRQELNTIASKPPRDHVFQNNFALKT 180
Db 121 DPLGYEDVPEADREGVIRYVGVGDAPRSEKSRQELNTIASKPPRDHVFQNNFALKT 180

RESULT 4
US-08-687-706-62
; Sequence 62, Application US/08687706
; Patent No. 5928892
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby

```

: TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
: NUMBER OF SEQUENCES: 62
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Patrea L. Pabst
: STREET: 2800 One Atlantic Center
: STREET: 1201 West Peachtree Street
: CITY: Atlanta
: STATE: Georgia
: COUNTRY: USA
: ZIP: 30309-3450
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/687,706
: FILING DATE: 03-JAN-1994
: CLASSIFICATION:
: CLASSIFICATION: G01-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/177,109
: FILING DATE: 03-JAN-1994
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Pabst, Patrea L.
: REGISTRATION NUMBER: 31,284
: REFERENCE/DOCKET NUMBER: WU 107 DIV
: THE INFORMATION CONTAINED HEREIN IS UNCLASSIFIED
: TELEPHONE: (404) 873-8794
: TELEFAX: (404) 873-8795
: INFORMATION FOR SEQ ID NO: 62:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 187 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEetical: NO
: US-08-687-706-62

Query Match 55.3%; Score 534; DB 2; Len 187
Best Local Similarity 55.6%; Prod No. 5,46-50;
Matches 104; Conservative 34; Mismatches 49; I

Oy 1 CPEQSDIAFLIDGSGSIIPHDPRMKFVSTVMEQLKKSKTK
Db 1 CPEQSDIVFLIDGSGSISSRNFTAMNFVAVISQRPSTPS
Oy 61 EFGNNPFRSLKPIQLLGRHTATGIRKYVRELFNITNGA
Db 61 EFRSTNPISLASHVQGLPTTATLQVHRLFNSTG
Oy 121 DPLGYEDVLPEDRGVRYVIGVDAPFSEKSPQELNTAS
Db 121 DLSLDYKDVLPADAAGIIRVAYGVGLAFQNRNWKELNDIAS
Oy 181 IQNQLE 187
Db 181 IQNQKKE 187

RESULT 5
PCT-US96-01314-60
: General 60, Application PC/TUS9601314
: GENERAL INFORMATION:
: APPLICANT: M. Amin Attaouat
: TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGR
: TITLE OF INVENTION: ANTAGONISTS
: NUMBER OF SEQUENCES: 78
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dr. Richardson P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: Massachusetts

```

```

COUNTRY: U.S.A.
ZIP: 02111-9864
COMPUTER: IBM PS/2 Model 502 or 55SX
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRIORITY DATA: 08/380,167
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/267001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
ADDRESS: 200 Massachusetts St.
INFORMATION FOR SEQ ID NO.: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-01314-60

Query Watch      55 34;   Score 534; DB 5; Length 187;
Best Local Similarity 55.64; Proc No. 5,46-50;
Matches 104; Conservative 34; Mismatches 49; Indels 0; Gaps 0;

QY    1 CPGQSDGDAFLIDGGSGIIPHDPRMKCFVSTWELQKSKXTLFLSMQYSSEFRIHFTFK 60
Db    1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY    1 CPQEQDITVFIDGGSGISSSNATMMFRAVISQFORPSTQFSLMQFSNKFQTHTFE 60
Db    1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY    61 EPQNPNRSLVKPTTOLLGRTHATGIRKYVRLELFMTNGARNAKPLILWTIDGKEFG 120
Db    61 EPRTSNPPELLASVHQLQGCTTYNTAQNVRHLFHSAGARDNAKLILVTIDGKGEG 120
QY    121 DPLGVEDIVPEADREGVIRYIGVDGFAPRESKDELNTASKPPRDHVFOVNNPALKT 180
Db    121 DSLDYKVDPMDAGGIIRYAIGVLGFONRSKMELNDLASKSPGEHIKFVEDFDALCK 180
QY    181 IQNLQKE 187
Db    181 IQNLQKE 187

RESULT 6
US-08-974-899-7
Sequence 7, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD14 Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDING ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Genentech
CURRENT APPLICATION DATA:

```

```

: TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
:
: NUMBER OF SEQUENCES: 62
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Patrea L. Pabst
: STREET: 2800 One Atlantic Center
: CITY: Atlanta
: STATE: Georgia
: COUNTRY: USA
:
: ZIP: 30309-3450
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/687,706
: APPLICATION DATE: 26-JUL-1996
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: FILING DATE: 03-JAN-1994
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Pabst, Patrea L.
: REGISTRATION NUMBER: 31,284
: REFERENCE/DOCKET NUMBER: MU 107 DIV
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (404) 873-8394
: TELEFAX: (404) 873-8795
:
: INFORMATION FOR SEQ ID NO: 62:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 187 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEITICAL: NO
:
: US-08-687-706-62
:
: Query Match 55.34; Score 534; DB 2; Length 187;
: Best Local Similarity 55.64; Pos Num 5, 46-50;
: Matches 104; Conservative 34; Mismatches 49; Indels 0; Gaps 0;
:
: QY 1 CPQRDSDAFLIDGGSGSIIPDFRPMKEFVSTWMLQKSKTFLSLMOVSEERHPTFK 60
: DB 1 CPQRQDVIPLIDGGSGSIISRRFATMMNFVAVIQSFQSFQSLMFSNKFQTHPTFE 60
:
: QY 61 EQPNQPNRSRSLKPTQLGRTHATGIRKYVRELFNITNGARQNAFLVLVITDGEKFG 120
: DB 61 EFRFTSNPLSLASVHQLOQYFYTATQNVHRLFLFASVGAARDATKLIVITDQKKG 120
:
: QY 121 PLQCYSDVIVPADRGVIRVYGVDGAPRFSKSRQRENTLASKPDRHVFQVFNFEALTK 180
: DB 121 DLSLDYKDVIPMAADAGIIRVAYGLVGFQPNRNSKNELNDLASKPSQEHFKVEDFALDK 180
:
: QY 181 IQNQLRE 187
: DB 181 IQNQLKE 187
:
: RESULT 5
: PCT-US96-01314-60
: Sequence 60, Application PC/TUG9601314
: GENERAL INFORMATION:
: APPLICANT: M. Amin Arnaut
: TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
: NUMBER OF SEQUENCES: 78
: CORRESPONDENCE ADDRESS:
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: Massachusetts

```



```

; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; INVENTOR: Lee, Wendy M.
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-974-899-7

Query Match 29.7%; Score 286.5; DB 3; Length 184;
Best Local Similarity 33.5%; Pred. No. 3.6e-23;
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;

Qy 7 DIAPLDGSGSIIPHDPRMKFVSTWBLKSKTFLSLMOVSEPRHFTFKFQNNP 66
Db 5 DLVFLDGSMSLQDFEKLIDPMKDVKKLSNTSYQFAAVQFSTSYKTFDFSDYVKRK 64
Qy 67 NPRLSVKPTITGLGRTATGIRKVVRELFNITNGARKNAKFLVITDGEKFCDDPLGYE 126
Db 65 DPDLALKHVMHLLNTFGAINVYATVFEELGARPDATKVLIIITDGE--ATDSGNI 122
Qy 127 DVTPEDAREGVIRVIGDFAFSEKSRQELNTASKPPRHHVQFVNNFEALKTIONQLR 186
Db 123 DAAKO-----IIVIGIGRHGFQTKESQETLHKFASKPASEFVKILDTPEKLDLFTLQ 177
Qy 187 EK 188
Db 178 KK 179

RESULT 7
US-09-795-798-7
; Sequence 7, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; REFERENCE/DOCKET NUMBER: P1014R1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-795-798-7

Query Match 29.7%; Score 286.5; DB 4; Length 184;
Best Local Similarity 33.5%; Pred. No. 3.6e-23;
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;

Qy 7 DIAPLDGSGSIIPHDPRMKFVSTWBLKSKTFLSLMOVSEPRHFTFKFQNNP 66
Db 5 DLVFLDGSMSLQDFEKLIDPMKDVKKLSNTSYQFAAVQFSTSYKTFDFSDYVKRK 64
Qy 67 NPRLSVKPTITGLGRTATGIRKVVRELFNITNGARKNAKFLVITDGEKFCDDPLGYE 126
Db 65 DPDLALKHVMHLLNTFGAINVYATVFEELGARPDATKVLIIITDGE--ATDSGNI 122
Qy 127 DVTPEDAREGVIRVIGDFAFSEKSRQELNTASKPPRHHVQFVNNFEALKTIONQLR 186
Db 123 DAAKO-----IIVIGIGRHGFQTKESQETLHKFASKPASEFVKILDTPEKLDLFTLQ 177
Qy 187 EK 188
Db 178 KK 179

RESULT 8
US-08-974-899-8
; Sequence 8, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; REFERENCE/DOCKET NUMBER: P1014R1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-974-899-8

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Query Match          29.2%; Score 281.5; DB 3; Length 184;
Best Local Similarity 33.0%; Pred. No. 1.3e-22;
Matches 60; Conservative 48; Mismatches 67; Indels 7; Gaps 2;

Qy 7 DIAFLDGSGLIIPDPRMKEFVSVMEQLKSKTFLSLMOYSSEFRIHFTKFPQNP 66
Db 5 DLIFPDGMSLQDFQKILDPKMDVKKLSNTSYQFAVQSTKTEFDFDQVQK 64

Qy 67 NPSLVKPIITOLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLGYE 126
Db 65 DPDALEHNVGEMLLNTFGALINYATEVFREELGARDPKTKVLIITDGS--ATDSGMI 122

Qy 127 DVTPADREGVIRVYGVGDADFSEKSRQELNTIASKPRDHYVFNNEALKTIONQLR 186
Db 123 DAAKD-----IIRVIIGIKGHFOTKESQETLHKFASKPASEFVKILDTPEKLDLPTELQ 177

Qy 187 EK 188
Db 178 KK 179

RESULT 9
; Sequence 9, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way, San Francisco
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-FEB-2001
; PRIORITY: 6703018 (Unknown)
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION SOURCE: Genentech
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-795-798-8
Query Match          29.2%; Score 281.5; DB 4; Length 184;
Best Local Similarity 33.0%; Pred. No. 1.3e-22;
Matches 60; Conservative 46; Mismatches 67; Indels 7; Gaps 2;

Qy 7 DIAFLDGSGLIIPDPRMKEFVSVMEQLKSKTFLSLMOYSSEFRIHFTKFPQNP 66
Db 5 DLIFPDGMSLQDFQKILDPKMDVKKLSNTSYQFAVQSTKTEFDFDQVQK 64

Qy 67 NPSLVKPIITOLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLGYE 126
Db 65 DPDALEHNVGEMLLNTFGALINYATEVFREELGARDPKTKVLIITDGS--ATDSGMI 122

Qy 127 DVTPADREGVIRVYGVGDADFSEKSRQELNTIASKPRDHYVFNNEALKTIONQLR 186
Db 123 DAAKD-----IIRVIIGIKGHFOTKESQETLHKFASKPASEFVKILDTPEKLDLPTELQ 177

Qy 187 EK 188
Db 178 KK 179

RESULT 10
; Sequence 10, Application PC/TUS9601314
; GENERAL INFORMATION:
; APPLICANT: M. Amin Athaout
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 of 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PC/TUS96/01314
; FILING DATE: 08-JAN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/380,167
; FILING DATE: 30-JAN-95
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/267001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION SOURCE: Unknown
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-01314-61

Query Match          27.6%; Score 266; DB 5; Length 181;
Best Local Similarity 33.0%; Pred. No. 6e-21;
Matches 60; Conservative 46; Mismatches 68; Indels 8; Gaps 3;

Qy 1 CPQSDSIAPLIDGSGSLIPDPRMKEFVSVMEQLKSKTFLSLMOYSSEFRIHFTK 60
Db 1 CIKGNVDFLVFDGMSLQDFQKILDPKMDVKKLSNTSYQFAVQSTKTEFDFD 60

Qy 61 BFOVNPRESLVKPIITOLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 61 DYVKKMDPDLAKHVKHMLLNTFGALINYATEVFREELGARDPKTKVLIITDGS--A 118

Qy 121 DPLGVGVIPDPRMKEFVSVMEQLKSKTFLSLMOYSSEFRIHFTKFPQNP 179
Db 119 TDSGNDAKD-----IIRVIIGIKGHFOTKESQETLHKFASKPASEFVKILDTPEK 173

Qy 180 TI 181

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DB 174 DL 175

RESULT 11
US-08-476-062A-50
; Sequence 10, Application US/08476062A
; Patent No. 5877275
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,062A
; FILING DATE: 07-JUN-1995
; PRIORITY DATE: 08/216,081
; APPLICATION NUMBER: 07/637,830
; FILING DATE: 04-JAN-1991
; APPLICATION NUMBER: 07/539,842
; FILING DATE: 18-JUN-1990
; APPLICATION NUMBER: 07/212,573
; FILING DATE: 28-JUN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/068003
; TELEPHONE: (617) 542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-476-062A-50

Query Match 17.7%; Score 171; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 NAFKILVITDGEKFGDPLGYEDVIEADREGV 137
DB 1 NAFKILVITDGEKFGDPLGYEDVIEADREGV 33

RESULT 12
PCT-US96-01314-50
; Sequence 10, Application PC/TUS9601114
; Patent No. 5877275
; GENERAL INFORMATION:
; APPLICANT: M. Amin Arnaout
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,062A
; FILING DATE: 07-JUN-1995
; PRIORITY DATE: 08/216,081
; APPLICATION NUMBER: 07/637,830
; FILING DATE: 21-MAR-1994
; APPLICATION NUMBER: 07/539,842
; FILING DATE: 04-JAN-1991
; APPLICATION NUMBER: 07/212,573
; FILING DATE: 28-JUN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/068003
; TELEPHONE: (617) 542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-476-062A-50

Query Match 17.7%; Score 171; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 NAFKILVITDGEKFGDPLGYEDVIEADREGV 137
DB 1 NAFKILVITDGEKFGDPLGYEDVIEADREGV 33

RESULT 13
US-08-476-062A-10
; Sequence 10, Application US/08476062A
; Patent No. 5877275
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,062A
; FILING DATE: 07-JUN-1995
; PRIORITY DATE: 08/216,081
; APPLICATION NUMBER: 07/637,830
; FILING DATE: 21-MAR-1994
; APPLICATION NUMBER: 07/539,842
; FILING DATE: 04-JAN-1991
; APPLICATION NUMBER: 07/212,573
; FILING DATE: 28-JUN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/068003
; TELEPHONE: (617) 542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-476-062A-10

Query Match 17.7%; Score 171; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 NAFKILVITDGEKFGDPLGYEDVIEADREGV 137
DB 1 NAFKILVITDGEKFGDPLGYEDVIEADREGV 33

CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRIOR APPLICATION DATA: 08/380,167
APPLICATION NUMBER: 07/637,830
FILING DATE: 21-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/267001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 33
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US96-01314-50

Query Match 17.7%; Score 171; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 NAFKILVITDGEKFGDPLGYEDVIEADREGV 137
DB 1 NAFKILVITDGEKFGDPLGYEDVIEADREGV 33

RESULT 13
US-08-476-062A-10
; Sequence 10, Application US/08476062A
; Patent No. 5877275
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,062A
; FILING DATE: 07-JUN-1995
; PRIORITY DATE: 08/216,081
; APPLICATION NUMBER: 07/637,830
; FILING DATE: 21-MAR-1994
; APPLICATION NUMBER: 07/539,842
; FILING DATE: 04-JAN-1991
; APPLICATION NUMBER: 07/212,573
; FILING DATE: 28-JUN-1988

ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/068003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-08-476-062A-10

Query Match 15.1%; Score 146; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.1e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 FKILVITDGKFDPLGYEDVPEADR 134
|||||

Db 1 FKILVITDGKFDPLGYEDVPEADR 28
|||||

RESULT 14
PCT-US96-01314-10
Sequence 10, Application PC/TUS9601314
GENERAL INFORMATION:
APPLICANT: M. Amin Arnaout
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
ANTAGONISTS
INVENTOR: M. Amin Arnaout
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/380,167
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/267001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US96-01314-10

Query Match 15.1%; Score 146; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.1e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 FKILVITDGKFDPLGYEDVPEADR 134
|||||

Db 1 FKILVITDGKFDPLGYEDVPEADR 28
|||||

RESULT 15
US-08-476-062A-8
Sequence 8, Application US/08476062A
Patent No. 5877275
GENERAL INFORMATION:
APPLICANT: Arnaout, M. Amin
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
RESPONSES WITH BETA2 INTEGRINS
INVENTOR: M. Amin Arnaout
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,062A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,081
FILING DATE: 21-MAR-1994
APPLICATION NUMBER: 07/637,830
FILING DATE: 04-JAN-1991
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 07/212,573
FILING DATE: 28-JUN-1986
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/068003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-08-476-062A-8

Query Match 13.4%; Score 129; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 PNPRLSVVITQLGRTHTATGIRK 90
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Db 1 PNPRLSVVITQLGRTHTATGIRK 25
|||||

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Job time : 44 secs

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OM protein - protein search, using sw model

Run on: November 14, 2005, 17:37:39 ; Search time 164 Seconds
(without alignments)
479.640 Million cell updates/sec

Title: US-09-758-493-1_COPY_1_188

Perfect score: 965
Sequence: 1 CPEQSDIAFLDGGSGIIP.....VFQVNFALQIQJREK 188

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Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:

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13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	939	97.3	184	15	US-10-346-863-37
4	534	55.3	184	15	US-10-615-515-9
5	333.5	34.6	176	20	US-11-000-473-59
6	286.5	29.7	182	15	US-09-758-782-38
7	286.5	29.7	182	15	US-10-346-863-33
8	286.5	29.7	183	15	US-10-346-863-20
9	286.5	29.7	183	15	US-10-346-863-41
10	286.5	29.7	183	16	US-10-615-515-4
11	286.5	29.7	184	10	US-09-795-798-7

Sequence 4, Appl
Sequence 17, Appl
Sequence 20, Appl
Sequence 7, Appl
Sequence 35, Appl
Sequence 36, Appl
Sequence 56, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 60, Appl
Sequence 40, Appl
Sequence 4, Appl
Sequence 16, Appl
Sequence 76, Appl
Sequence 28, Appl
Sequence 43, Appl
Sequence 31, Appl
Sequence 3, Appl
Sequence 130, Appl
Sequence 24, Appl
Sequence 81, Appl
Sequence 30, Appl
Sequence 22, Appl
Sequence 50, Appl
Sequence 1209, Appl
Sequence 27, Appl
Sequence 29, Appl
Sequence 8, Appl
Sequence 31, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 3310, A
Sequence 47637, A

ALIGNMENTS

US-10-346-863-17
Sequence 17, Application US/10346863
Publication No. US20040038325A1
GENERAL INFORMATION:
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
APPLICANT: GUTTERIDGE, ALEX
TITLE OF INVENTION: ADHESION MOLECULES
PUBLICATION NO.: US20040038325A1
CURRENT APPLICATION NUMBER: US/10/346,863
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: PCT/GB01/03318
PRIOR FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: GB 0018126.3
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: GB 0025447.4
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 184
LENGTH: 184
TYPE: PPT
ORGANISM: Homo sapiens
US-10-346-863-17

Query Match 97.3%; Score 939; DB 15; Length 184;
Best Local Similarity 100.0%; Prad. No. 7.3e-92;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 DSDIAFLDGGSGIIPHDPRMKVSTVMEQKSKTLFSLMOYSEPRIFHTFKFQ 64
DB 1 DSDIAFLDGGSGIIPHDPRMKVSTVMEQKSKTLFSLMOYSEPRIFHTFKFQ 60

Qy 65 NPNPRLVPEITQLGRTHATGIRKVVRELFNTNGAKNAFKILVITDGEKFGDPLG 124
Db 61 NPNPRLVPEITQLGRTHATGIRKVVRELFNTNGAKNAFKILVITDGEKFGDPLG 120
Qy 125 YEDVIPADREGVIRVVGCDAFRSKRSQELNTIASKPRDHVFOVNNFEALKTIONQ 184
Db 121 YEDVIPADREGVIRVVGCDAFRSKRSQELNTIASKPRDHVFOVNNFEALKTIONQ 180
Qy 185 LREK 188
Db 181 LREK 184

RESULT 2
US-10-346-863-37
; Sequence 9: Application US/10346863
; Publication No. US2004003825A1
; GENERAL INFORMATION:
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: FAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346,863
; PRIOR FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: PCT/G801/03118
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: GB 0018126.3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447.4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-346-863-37

Query Match 97.3%; Score 919; DB 15; Length 187;
Best Local Similarity 100.0%; Pred. No. 7,5e-92;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DSDIAPLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTKEFON 64
Db 1 DSDIAPLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTKEFON 60
Qy 65 NPNPRLVPEITQLGRTHATGIRKVVRELFNTNGAKNAFKILVITDGEKFGDPLG 124
Db 61 NPNPRLVPEITQLGRTHATGIRKVVRELFNTNGAKNAFKILVITDGEKFGDPLG 120
Qy 125 YEDVIPADREGVIRVVGCDAFRSKRSQELNTIASKPRDHVFOVNNFEALKTIONQ 184
Db 121 YEDVIPADREGVIRVVGCDAFRSKRSQELNTIASKPRDHVFOVNNFEALKTIONQ 180
Qy 185 LREK 188
Db 181 LREK 184

RESULT 3
US-10-615-515-9
; Sequence 9: Application US/10615515
; Publication No. US2004013297A1
; GENERAL INFORMATION:
; APPLICANT: FAGAN, RICHARD, JOSEPH
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2004
; CURRENT APPLICATION NUMBER: US/10/615,515
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: PCT/G802/00107

; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: GB 0100750.9
; PRIOR FILING DATE: 2001-01-11
; PUBLICATION NO. US2004003825A1
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-615-515-9

Query Match 97.3%; Score 919; DB 16; Length 187;
Best Local Similarity 100.0%; Pred. No. 7,5e-92;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DSDIAPLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTKEFON 64
Db 1 DSDIAPLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTKEFON 60
Qy 65 NPNPRLVPEITQLGRTHATGIRKVVRELFNTNGAKNAFKILVITDGEKFGDPLG 124
Db 61 NPNPRLVPEITQLGRTHATGIRKVVRELFNTNGAKNAFKILVITDGEKFGDPLG 120
Qy 125 YEDVIPADREGVIRVVGCDAFRSKRSQELNTIASKPRDHVFOVNNFEALKTIONQ 184
Db 121 YEDVIPADREGVIRVVGCDAFRSKRSQELNTIASKPRDHVFOVNNFEALKTIONQ 180
Qy 185 LREK 188
Db 181 LREK 184

RESULT 4
US-11-000-473-59
; Sequence 59: Application US/11000473
; Publication No. US2005027256A1
; GENERAL INFORMATION:
; APPLICANT: ARMOUR, M. Armin
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN ANTAGONISTS
; FILE REFERENCE: 00786-267002
; CURRENT APPLICATION NUMBER: US/11/000,473
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US/09/592,617
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 08/380,167
; PRIOR FILING DATE: 1999-01-30
; PRIOR APPLICATION NUMBER: US 08/216,081
; PRIOR FILING DATE: 1994-02-21
; PRIOR APPLICATION NUMBER: US 07/637,830
; PRIOR FILING DATE: 1991-01-04
; PRIOR APPLICATION NUMBER: US 07/539,842
; PRIOR FILING DATE: 1990-06-18
; PRIOR APPLICATION NUMBER: US 07/212,573
; PRIOR FILING DATE: 1988-06-28
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-473-59

Query Match 55.3%; Score 534; DB 20; Length 187;
Best Local Similarity 55.6%; Pred. No. 1.5e-48;
Matches 104; Conservative 34; Mismatches 49; Indels 0; Gaps 0;

Qy 1 CPQDSDIAPLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTKE 60
Db 1 CPQDSDIAPLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTKE 60
Qy 61 EFOONNPRLVPEITQLGRTHATGIRKVVRELFNTNGAKNAFKILVITDGEKFG 120
Db 61 EFRNTSNPLSLASVHQLQGFVTTATATQNVVHFLFASVGAARDATKILVITDGEKFG 120

```
Qy 121 DPLGVDEVPDEADREGVIRYVIGVDAPFSEKSRQELNTASKPPDRHVFQVNNFPAKLT 180
Db 121 DSLQDKVIMADAGIIRYALVGLAFQNSWKNELDIASKRSQEHFKVDFEDLKD 180
Qy 181 IQNQLRE 187
Db 181 IQNQLKE 187

RESULT 5
US-09-976-782-38
; Sequence 38, Application US/09976782
; Publication No. US20010190715A1
; GENERAL INFORMATION:
; APPLICANT: Grosse et al
; TITLE OF INVENTION: NO. US20030190715A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-157
; CURRENT APPLICATION NUMBER: US/09/976.782
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240.113
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240.662
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240.732
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240.625
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240.703
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/241.190
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240.637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240.669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262.455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240.648
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence:Consensus
US-09-976-782-38

Query Match 34.6%; Score 333.5; DB 10; Length 176;
Best Local Similarity 43.4%; Pred. No. 3.6e-27;
Matches 79; Conservative 29; Mismatches 65; Indels 9; Gaps 4;

Qy 7 DIAPLDGSGSIIPHDPRRMKEFVSTVMEQLKSKTKLFLSLMOYSEBFRHHTFKFQNP 64
Db 1 DVLPLDGGSGIGQNFQVDFVVERLDIGDKRVGLVQISDNRTEFLANDIQN 60
Qy 65 NNPRESLVKPTQL-LGTHHTATGIRKVVRLFNITNGARKNAKPLVITDGSKFGDPL 123
Db 61 KDEVLQALKIOYGGGCTGTGALQVYVVRNLFTASGSGEGAPKVLVLIDGSCDDPI 120
Qy 124 GVEDVPEADREGVIRYVIGVDAPFSEKSRQELNTASKPPDRHVFQVNNFPAKLTQ 183
Db 121 --RDVLNMLKKAGVNVFAIGVGNADNVE---ELREIASKPDQEHVPKVSDFEALDTI 174
Qy 184 QL 185
Db 175 LL 176
```

RESULT 6

```
US-10-346-863-33
; Sequence 33, Application US/10346863
; Publication No. US20040038325A1
; GENERAL INFORMATION:
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: FAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346.863
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: PCT/GB01/03318
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0018126.3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447.4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-346-863-33

Query Match 29.7%; Score 286.5; DB 15; Length 182;
Best Local Similarity 33.5%; Pred. No. 2e-24;
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;

Qy 7 DIAPLDGSGSIIPHDPRRMKEFVSTVMEQLKSKTKLFLSLMOYSEBFRHHTFKFQNP 66
Db 4 DVLPLDGGSGIAPDFQKILDPKQVNMKLSNTSYQFAAVQFSTSYKTFDFSDYVKRK 63
Qy 67 NPSLVKPTQLGTHHTATGIRKVVRLFNITNGARKNAKPLVITDGSKFGDPLGYE 126
Db 64 DFDALKHVMILLTNTFGALNTVATEVPFRELGAAPDATKVLIIITDGE--ATDSGT 121
Qy 127 DYTEADREGVIRYVIGVDAPFSEKSRQELNTASKPPDRHVFQVNNFPAKLTQNL 186
Db 122 DAAXD----LIRYIIGIRKHPQTKESQETLHKFASKPASEFVKILDTPEKLNLFTELQ 176
Qy 187 EK 188
Db 177 KK 178

RESULT 7
US-10-346-863-20
; Sequence 20, Application US/10346863
; Publication No. US20040038325A1
; GENERAL INFORMATION:
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: FAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346.863
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: PCT/GB01/03318
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0018126.3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447.4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-346-863-20

Query Match 29.7%; Score 286.5; DB 15; Length 183;
```

Best Local Similarity 33.5%; Pred. No. 4e-22;
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;
Qy 7 DIAPLIDGSGSIIPHDFRMKEFVSTWQKLSKTLPSLMQYSEERHFTKFNPNP 66
Db 4 DLVFLFGSGNSLQDFEQKILDMKDKVKKLSNTSYQAAVQFSTSKTEFDSFYVKK 63
Qy 67 NPRLSVKPTTOLLGRTHATGIRKVVRELPNITNGARKNAFKILVITDGEKFDPLGYE 126
Db 64 DPALLKHVGMHLLNTFGAINVATEVFRELGPDPATKVLIIITDGE--ATDSGNI 121
Qy 127 DVIPEDREGVIRYVIGVDAPFSEKSEKRELNTIASKPRDHVFNPNFEALKTIONOLR 186
Db 122 DAADK-----IIRYIGIGKHGFQTESQETLHKFASKPASEFVKILDTPEKLDLPTELQ 176
Qy 187 EK 188
Db 177 KK 178

RESULT 8
US-10-346-863-41
; Sequence 41, Application US/10346863
; Publication No. US2004003925A1
; GENERAL INFORMATION:
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: PHILLIPS, CHRISTOPHER BENJAMIN
; APPLICANT: PAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346.863
; PRIOR FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: PCT/GB01/03318
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0018126.3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447.4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-346-863-41

Query Match 29.7%; Score 286.5; DB 15; Length 183;
Best Local Similarity 33.5%; Pred. No. 4e-22;
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;
Qy 7 DIAPLIDGSGSIIPHDFRMKEFVSTWQKLSKTLPSLMQYSEERHFTKFNPNP 66
Db 4 DLVFLFGSGNSLQDFEQKILDMKDKVKKLSNTSYQAAVQFSTSKTEFDSFYVKK 63
Qy 67 NPRLSVKPTTOLLGRTHATGIRKVVRELPNITNGARKNAFKILVITDGEKFDPLGYE 126
Db 64 DPALLKHVGMHLLNTFGAINVATEVFRELGPDPATKVLIIITDGE--ATDSGNI 121
Qy 127 DVIPEDREGVIRYVIGVDAPFSEKSEKRELNTIASKPRDHVFNPNFEALKTIONOLR 186
Db 122 DAADK-----IIRYIGIGKHGFQTESQETLHKFASKPASEFVKILDTPEKLDLPTELQ 176
Qy 187 EK 188
Db 177 KK 178

RESULT 9
US-10-615-515-7
; Sequence 7, Application US/10615515
; Publication No. US200400413297A1
; GENERAL INFORMATION:
; APPLICANT: PAGAN, RICHARD, JOSEPH

; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2004 US/10/615.515
; CURRENT APPLICATION NUMBER: US/10/615.515
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/GB02/00107
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: GB 0100750.9
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-615-515-7

Query Match 29.7%; Score 286.5; DB 16; Length 183;
Best Local Similarity 33.5%; Pred. No. 4e-22;
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;
Qy 7 DIAPLIDGSGSIIPHDFRMKEFVSTWQKLSKTLPSLMQYSEERHFTKFNPNP 66
Db 4 DLVFLFGSGNSLQDFEQKILDMKDKVKKLSNTSYQAAVQFSTSKTEFDSFYVKK 63
Qy 67 NPRLSVKPTTOLLGRTHATGIRKVVRELPNITNGARKNAFKILVITDGEKFDPLGYE 126
Db 64 DPALLKHVGMHLLNTFGAINVATEVFRELGPDPATKVLIIITDGE--ATDSGNI 121
Qy 127 DVIPEDREGVIRYVIGVDAPFSEKSEKRELNTIASKPRDHVFNPNFEALKTIONOLR 186
Db 122 DAADK-----IIRYIGIGKHGFQTESQETLHKFASKPASEFVKILDTPEKLDLPTELQ 176
Qy 187 EK 188
Db 177 KK 178

RESULT 10
US-09-805-354-4
; Sequence 4, Application US/09805354
; Publication No. US2003007875A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; FILE REFERENCE: US/09/805.354
; FILE REFERENCE: US/09/805.354
; CURRENT APPLICATION NUMBER: US/09/805.354
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-354-4

Query Match 29.7%; Score 286.5; DB 10; Length 184;
Best Local Similarity 33.0%; Pred. No. 4.1e-22;
Matches 62; Conservative 49; Mismatches 70; Indels 7; Gaps 2;
Qy 1 CPQEDSDIAPLIDGSGSIIPHDFRMKEFVSTWQKLSKTLPSLMQYSEERHFTKFNPNP 60
Db 1 CTKGNDLVFLFGSGNSLQDFEQKILDMKDKVKKLSNTSYQAAVQFSTSKTEFDSFYVKK 60
Qy 61 EFNQNNPRLSVKPTTOLLGRTHATGIRKVVRELPNITNGARKNAFKILVITDGEKFDPLGYE 120

Db 61 DYVKWDPDALLKGVHMLLNTTGAIVYATVYFRELGARPDATKVLIIITDGE--A 118
Qy 121 DPLGVGVIPADREGVIRYVGVDAFRSEKSEQLNTIASPPRDHVFQVNNFALKT 180
Db 119 TDSGNIDAOK-----IIRYIIGIKGFOTKESQETLHKFASKPASEFVKLITDFEKLKD 173
Qy 181 IQNQLREK 188
Db 174 LFTLEQKK 181

RESULT 11

US-09-795-798-7
; Sequence 7, Application US/09795798
; Publication No. US20030207336A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 18-FEB-2001
; CLASSIFICATION: Unknown
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: Unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P101481
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION CONTAINED HEREIN IS UNCLASSIFIED
; DATE 08-28-2001 BY 60322 UCBAW/SJS
; SEQUENCE CHARACTERISTICS:
; TYPE: Amino Acid
; LENGTH: 184 amino acids
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-795-798-7

Query Match 29.7%; Score 286.5; DB 10; Length 184;
Best Local Similarity 33.5%; Pred. No. 4.1e-22;
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;
Qy 7 DIADLDGSGIIPDPRKKEFVSTWEOQLKSKTKLPSLMQYSEFRHHTFTKFNQNP 66
Db 5 DLVFLDGSNSLQDFQKILDFPMKDVWKKLSNTSYQFAAVQFSTVKTDFSDYVKKR 64
Qy 67 NPSRLVKPITQLGRTHATGIRKVVRELFWITNGARKNAFKILVITDGEKFDPLGYE 126
Db 65 DFDALKHVGIMLLNTTGAIVYATVYFRELGARPDATKVLIIITDGE--ATDSGNI 122
Qy 127 DVIFPADREGVIRYVGVDAFRSEKSEQLNTIASPPRDHVFQVNNFALKTIONLR 186
Db 123 DAKO-----IIRYIIGIKGFOTKESQETLHKFASKPASEFVKLITDFEKLKDLPTELQ 177
Qy 187 EK 188
Db 178 KK 179

RESULT 12

US-09-758-493-4
; Sequence 4, Application US/09758493
; Publication No. US20040086935A1
; GENERAL INFORMATION:
; APPLICANT: Arnaud, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
; FILE REFERENCE: 00786-804001
; CURRENT APPLICATION NUMBER: US/09/758,493
; PENDING FILING DATE: 2801-01-11
; PRIOR FILING DATE: 2000-07-31
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-493-4

Query Match 29.7%; Score 286.5; DB 11; Length 184;
Best Local Similarity 33.0%; Pred. No. 4.1e-22;
Matches 62; Conservative 49; Mismatches 70; Indels 7; Gaps 2;
Qy 1 CPQSDSDIADLDGSGIIPDPRKKEFVSTWEOQLKSKTKLPSLMQYSEFRHHTFTK 60
Db 1 CIKGNVLDVFLFDGSNSLQDFQKILDFPMKDVWKKLSNTSYQFAAVQFSTVKTDFDS 60
Qy 61 EFQNNPNSLVKPIITQLGRTHATGIRKVVRELFWITNGARKNAFKILVITDGEKFG 120
Db 61 DYVKWDPDALLKGVHMLLNTTGAIVYATVYFRELGARPDATKVLIIITDGE--A 118
Qy 121 DPLGVGVIPADREGVIRYVGVDAFRSEKSEQLNTIASPPRDHVFQVNNFALKT 180
Db 119 TDSGNIDAOK-----IIRYIIGIKGFOTKESQETLHKFASKPASEFVKLITDFEKLKD 173
Qy 181 IQNQLREK 188
Db 174 LFTLEQKK 181

RESULT 13

US-10-144-259-4
; Sequence 4, Application US/10144259
; Publication No. US20030109631A1
; GENERAL INFORMATION:
; APPLICANT: Arnaud, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-548001
; CURRENT APPLICATION NUMBER: US/10/144,259
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PENDING FILING DATE: 2801-01-11
; PRIOR FILING DATE: 2000-07-31
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-259-4

Query Match 29.7%; Score 286.5; DB 14; Length 184;
Best Local Similarity 33.0%; Pred. No. 4.1e-22;
Matches 62; Conservative 49; Mismatches 70; Indels 7; Gaps 2;

QY	1	CPQEDSDIAPLIDGSGSIIPHDFRMKBEFVSTVMEOLKKGKTLFSLMOYSEEFRIHTFK	60
DB	1	CTKGNVDLVPFGMGSQDEBFKILIDPMKMDKNGKLSSTVFAAFQESTSVKTFEFS	60
QY	61	EPQNNPNSFVPIPTQLGRTHTATCIKRVQELNPTNGARKNKLITVOTGSEK	120
DB	61	DYVMMQDALLAHKVMULLNTFGAIINYVATEVFREELGARDPATKVLIIITDGE	118
QY	121	DPYAGEDVIPAEOREVIRVITGVGDAPSEKSGREBLNTIASKPPHDFVQNNNEALK	180
DB	119	TUSGNIDAOK-----IIRYIGIKRHFOETSEQTLHKPASKPASEFKILDTFSEKLD	173
QY	181	IONLESEK	188
DB	174	LFELOKK	181

RESULT 14

US-10-473-127-2033
Sequence 2033 Application US/10473127

; sequence 2033, Application US/1
: Publication No. US20040236091A1; PUBLICATION NO. US20
: GENERAL INFORMATION:

APPLICANT: ZYCOB INC.

TITLE OF INVENTION: TRAN

; FILB REFERENCE: 08191-02

; CURRENT APPLICATION NUMBER; US/10/473,127

; CURRENT PILING DATE: 2003-01-01

; PRIOR APPLICATION NUMBER: 601
 ; PRIOR FILING DATE: 2001-03-21

;; PRIOR FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60

; PRIOR APPLICATION NUMBER: 60-
; PRIOR FILING DATE: 2001-05-2

; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/

PRIOR FILING DATE: 2001-08-01

10 ; PRIOR APPLICATION NUMBER: 60,

; PRIOR FILING DATE: 2001-10-0

; PRIOR APPLICATION NUMBER: 60

; PRIOR FILING DATE: 2001-12-01
; PRIOR APPLICATION NUMBER: 60

; PRIOR APPLICATION NUMBER: 60;
; PRIOR FILING DATE: 2002-02-2

;; PRIOR FILING DATE: 2002-02-2
: NUMBER OF SEQ ID NOS: 2041

; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FASTSEQ for Windows

; SEQ ID NO 2033

; LENGTH: 184

; TYPE: PRT

; ORGANISM: HO

US-10-473-127-2033

Query Match

Query match
Best local similarity

Query Match 29.7%; Score 286.5; DB 16; Length 184;
Best Local Similarity 33.5%; Pred. No. 4.1e-22;
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;

RESULT 15

US-10-727-737-7

; Sequence 7, Application US/10727737

; Publication No. US20040146507A1

GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
CITY: San Francisco
STATE: South San Francisco
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: GENENTECH DATA (Genentech)
CURRENT PUBLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: M. M. M.
REGISTRATION NUMBER: 40,378
REFERENCES/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: Amino Acid
ORGANISM: HUMAN
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
18-10-727-737-7

[illegible]

Search completed: November 14, 2005, 17:51:39
Job time : 166 secs

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